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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 04/26/2001

PATENT APPLICATION: US/09/030,482B

TIME: 11:56:25

Input Set : D:\38109-20007.00 seqlist (final)!.txt

Output Set: N:\CRF3\04262001\I030482B.raw

ENTERED

4 <110> APPLICANT: Snutch, Terry
 5 NeuroMed Technologies, Inc.
 7 <120> TITLE OF INVENTION: NOVEL HUMAN CALCIUM CHANNELS AND RELATED
 8 PROBES, CELL LINES AND METHODS
 11 <130> FILE REFERENCE: 38109-20007.00
 13 <140> CURRENT APPLICATION NUMBER: US 09/030,482B
 14 <141> CURRENT FILING DATE: 1998-02-25
 16 <150> PRIOR APPLICATION NUMBER: US 60/039,204
 17 <151> PRIOR FILING DATE: 1997-02-28
 19 <160> NUMBER OF SEQ ID NOS: 33
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 24
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Rat
 28 <400> SEQUENCE: 1
 29 gtcaaaaactc aggccttcta ctgg 24
 31 <210> SEQ ID NO: 2
 32 <211> LENGTH: 24
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Rat
 36 <400> SEQUENCE: 2
 37 aacgtgttct tggctatcgc ggtg 24
 39 <210> SEQ ID NO: 3
 40 <211> LENGTH: 24
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Rat
 44 <400> SEQUENCE: 3
 45 gtgaaagcac agagcttcta ctgg 24
 47 <210> SEQ ID NO: 4
 48 <211> LENGTH: 24
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Rat
 52 <400> SEQUENCE: 4
 53 aacgttttct tggccattgc tgtg 24
 55 <210> SEQ ID NO: 5
 56 <211> LENGTH: 24
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Rat
 60 <400> SEQUENCE: 5
 61 gttaaatacca acgtcttcta ctgg 24
 63 <210> SEQ ID NO: 6
 64 <211> LENGTH: 24
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Rat
 68 <400> SEQUENCE: 6
 69 aatgtgttct tggccattgc ggtg 24

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71 <210> SEQ ID NO: 7
72 <211> LENGTH: 24
73 <212> TYPE: DNA
74 <213> ORGANISM: Rat
76 <400> SEQUENCE: 7
77 gtgaagtcctg tcacgtttta ctgg                24
79 <210> SEQ ID NO: 8
80 <211> LENGTH: 24
81 <212> TYPE: DNA
82 <213> ORGANISM: Rat
84 <400> SEQUENCE: 8
85 aagctcttct tggccattgc tgta                24
87 <210> SEQ ID NO: 9
88 <211> LENGTH: 24
89 <212> TYPE: DNA
90 <213> ORGANISM: Rat
92 <400> SEQUENCE: 9
93 gtcaagtcgc aagtgttcta ctgg                24
95 <210> SEQ ID NO: 10
96 <211> LENGTH: 24
97 <212> TYPE: DNA
98 <213> ORGANISM: Rat
100 <400> SEQUENCE: 10
101 aatgtattct tggctatcgc tgtg                24
103 <210> SEQ ID NO: 11
104 <211> LENGTH: 21
105 <212> TYPE: DNA
106 <213> ORGANISM: Rat
108 <400> SEQUENCE: 11
109 atctaygcyr tsatyggsat g                    21
111 <210> SEQ ID NO: 12
112 <211> LENGTH: 20
113 <212> TYPE: DNA
114 <213> ORGANISM: Rat
116 <400> SEQUENCE: 12
117 atggacaayt tygastaytc                    20
119 <210> SEQ ID NO: 13
120 <211> LENGTH: 168
121 <212> TYPE: DNA
122 <213> ORGANISM: Human
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Expressed sequence tag H55225
127 <400> SEQUENCE: 13
128 gtgatcactc tggaaggctg ggtggagatc atgtactacg tgatggatgc tcaactccttc        60
129 tacaacttca tctacttcat cctgcttata ataccctct tgccttgac cccatattgt        120
130 cttcccagag tgagctcatc cacctcgtca tgccctgactc gacgttca                    168
132 <210> SEQ ID NO: 14
133 <211> LENGTH: 98
134 <212> TYPE: DNA

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```

135 <213> ORGANISM: Human
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Expressed sequence tag H55617
140 <400> SEQUENCE: 14
141 gatggtcgag tactccctgg accttcagaa catcaacctg tcagccatcc gcaccgtgcg      60
142 cgtcctgagg cccctcaaag ccatcaaccg cgtgccca                               98
144 <210> SEQ ID NO: 15
145 <211> LENGTH: 94
146 <212> TYPE: DNA
147 <213> ORGANISM: Human
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Expressed sequence tag H55223
152 <400> SEQUENCE: 15
153 catgctggtg atcctgctga actgcgtgac acttggcatg taccagccgt gcgacgacat      60
154 ggactgcctg tccgaccgct gcaagatcct gcag                               94
156 <210> SEQ ID NO: 16
157 <211> LENGTH: 123
158 <212> TYPE: DNA
159 <213> ORGANISM: Human
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Expressed sequence tag H55544
164 <400> SEQUENCE: 16
165 gtatctctgg ttactttagt agccaacact cttggctact cagaccttgg tcccattaaa      60
166 tccctgcgaa ccttgagagc actaagacct ctaagagctt tgtctagatt tgaaggaatg      120
167 agg                                                                    123
169 <210> SEQ ID NO: 17
170 <211> LENGTH: 343
171 <212> TYPE: DNA
172 <213> ORGANISM: Human
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Expressed sequence tag F07776
177 <221> NAME/KEY: misc_feature
178 <222> LOCATION: (1)...(343)
179 <223> OTHER INFORMATION: n = A,T,C or G
181 <400> SEQUENCE: 17
182 ttctctccat tgtaggaatg tttctggctg aactgataga aaagtatatt gtgtgcoccta      60
W--> 183 ccctgttncg agtgatccgt cttgccagga ttggccgaat cctacgtctg atcaaaggag      120
184 caaaggggat ccgcacgctg ctctttgctt tgatgatgtc ccttcctgcg ttgtttaaca      180
W--> 185 tcggnctcct tcttttcctg gtcattgttca tctacgncat ctttgggatg tccaattttg      240
W--> 186 cctatgttaa gagggaagt gggatcgatg acatgttnan ctttgagacc tttggcaaca      300
187 gcatgatctg cctgttccaa attacaacct ctgctggctg gga                        343
189 <210> SEQ ID NO: 18
190 <211> LENGTH: 5562
191 <212> TYPE: DNA
192 <213> ORGANISM: Human
194 <220> FEATURE:
195 <221> NAME/KEY: CDS
196 <222> LOCATION: (1)...(5562)
197 <223> OTHER INFORMATION: Human alpha-1 partial sequence from BAC bK206c7

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```

199 <400> SEQUENCE: 18
200 atg ttt ttc gtc tca gcc aat ccc tgg gtg agt ttc acc agt ttt gat      48
201 Met Phe Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp
202 1 5 10 15
204 tta aac gtg gcc aat atg gac aac ttc ttc gcc ccc gtt ttc acc atg      96
205 Leu Asn Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met
206 20 25 30
208 ggc aaa tat tat acg caa ggc gac aag gtg ctg atg ccg ctg gcg att      144
209 Gly Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile
210 35 40 45
212 cag gct ctg aaa cag ctg atg ttc aaa ttg gtg gcc act gtt gct cga      192
213 Gln Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg
214 50 55 60
216 aca cat gct aca ccg tca cac atc acg ggt ggt cct gga aca ggg atg      240
217 Thr His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met
218 65 70 75 80
220 cac acg ggc acc ttc cag gaa gga gct gag cct ggt tca tct cag cac      288
221 His Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His
222 85 90 95
224 cct gag gca cag gcc acg tat aca gca ggg tgc acc cca gcc ccc acg      336
225 Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr
226 100 105 110
228 ggc gat ccc acc tgc tgc ttt gtc ctt gac ttg gtg tgc acg tgg ttt      384
229 Gly Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe
230 115 120 125
232 gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt ggc      432
233 Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly
234 130 135 140
236 atg tac cag ccg tgc gac gac atg gac tgc ctg tcc gac cgc tgc aag      480
237 Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys
238 145 150 155 160
240 atc ctg cag gtc ttt gat gac ttc atc ttt atc ttc ttt gcc atg gag      528
241 Ile Leu Gln Val Phe Asp Asp Phe Ile Phe Phe Phe Ala Met Glu
242 165 170 175
244 atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc tac      576
245 Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr
246 180 185 190
248 ctc ggg gac aca tgg aac cgc ctg gat ttc ttc atc gtc atg gca ggc      624
249 Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly
250 195 200 205
252 aac atc aac ctg tca gcc atc cgc acc gtg cgc gtc ctg agg ccc ctc      672
253 Asn Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
254 210 215 220
256 aaa gcc atc aac cgc gtg ccc agt atg cgg atc ctg gtg aac ctg ctc      720
257 Lys Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Asn Leu Leu
258 225 230 235 240
260 ctg gac aca ctg ccc atg ctg ggg aat gtc ctg ctg ctc tgc ttc ttt      768
261 Leu Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe
262 245 250 255

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```

264 gtc ttc ttc atc ttt ggc atc ata ggt gtg cag ctc tgg gcg ggc ctg      816
265 Val Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala Gly Leu
266                260                265                270
268 ctg cgt aac cgc tgc ttc ctg gag gag aac ttc acc ata caa ggg gat      864
269 Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp
270                275                280                285
272 gtg gcc ttg ccc cca tac tac cag ccg gag gag gat gat gag atg ccc      912
273 Val Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro
274                290                295                300
276 ttc atc tgc tcc ctg tcg ggc gac aat ggg ata atg ggc tgc cat gag      960
277 Phe Ile Cys Ser Leu Ser Gly Asp Asn Gly Ile Met Gly Cys His Glu
278 305                310                315                320
280 atc ccc ccg ctc aag gag cag ggc cgt gag tgc tgc ctg tcc aag gac      1008
281 Ile Pro Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp
282                325                330                335
284 gac gtc tac gac ttt ggg gcg ggg cgc cag gac ctc aat gcc agc ggc      1056
285 Asp Val Tyr Asp Phe Gly Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly
286                340                345                350
288 ctc tgt gtc aac tgg aac cgt tac tac aat gtg tgc cgc acg ggc agc      1104
289 Leu Cys Val Asn Trp Asn Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser
290                355                360                365
292 gcc aac ccc cac aag ggt gcc atc aac ttt gac aac atc ggt tat gct      1152
293 Ala Asn Pro His Lys Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala
294                370                375                380
296 tgg att gtc atc ttc cag gtg atc act ctg gaa ggc tgg gtg gag atc      1200
297 Trp Ile Val Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Glu Ile
298 385                390                395                400
300 atg tac tac gtg atg gat gct cac tcc ttc tac aac ttc atc tac ttc      1248
301 Met Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe
302                405                410                415
304 atc ctg ctt atc ata agt gag ctc atc cac ctc gtc atg cct gac tgc      1296
305 Ile Leu Leu Ile Ile Ser Glu Leu Ile His Leu Val Met Pro Asp Cys
306                420                425                430
308 agc ttc agc aca gca cag tcc cca aaa tgt caa ggt gat tca ctc cca      1344
309 Ser Phe Ser Thr Ala Gln Ser Pro Lys Cys Gln Gly Asp Ser Leu Pro
310                435                440                445
312 gga gtc gct gct gaa tcc ctg ctg ctg cga gac tct agc tcc tca gtc      1392
313 Gly Val Ala Ala Glu Ser Leu Leu Leu Arg Asp Ser Ser Ser Ser Val
314                450                455                460
316 atc act gat gag gct gca gcc atg gag aac ctc ctg gcg ggc acc tcc      1440
317 Ile Thr Asp Glu Ala Ala Ala Met Glu Asn Leu Leu Ala Gly Thr Ser
318 465                470                475                480
320 aag ggg gat gaa agc tat ctg ctc agg ctg gcc ggc agc caa gtt cac      1488
321 Lys Gly Asp Glu Ser Tyr Leu Leu Arg Leu Ala Gly Ser Gln Val His
322                485                490                495
324 tcc cag gct cag caa atg ctg ggg agg ggg ctg ggc cct gaa agc ctg      1536
325 Ser Gln Ala Gln Gln Met Leu Gly Arg Gly Leu Gly Pro Glu Ser Leu
326                500                505                510
328 gaa act gga gag gag ccc cac tcg tgg agc cct cgg gcc aca agg aga      1584

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 04/26/2001

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Input Set : D:\38109-20007.00 seqlist (final)!.txt

Output Set: N:\CRF3\04262001\I030482B.raw

L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33